

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (iii) NUMBER OF SEQUENCES: 16
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 963 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: N
 - (iv) ANTI-SENSE: N
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pTrimer(T0)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 12..947
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

Hind III

BglII

AAGCTTACGTAAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCG
CGGTCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGACCTCCT
GGTCCCCCTGGTCCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCAC
CTCAAGAGAAGGCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGT
GGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAG
ATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCCCGCACCTGCC
GTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCC
CAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGT
GAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCA
GCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGG
ATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAG
CTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACT
GCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCT
GCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTC
ACCTACAGCGTCACTGTGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGA
CAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGC

CCCCTTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTC
TGCTTCCTGTAAACTCCCTCCATCTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

1	RSNGLPGPIG	PPGPRGRTGD	AGPVGPPGPP	GPPGPPGPPS	AGFDFSFLPQ	PPQEKAHDGG	60
61	RYRADDANV	VRDRDLEVD	TLKSLSQQIE	NIRSPEGSRK	NPARTCRDLK	MCHSDWKSGE	120
121	YWIDPNQCN	LDAIKVFCNM	ETGETCVYPT	QPSVAQKNWY	ISKNPKDKRH	VWFGESMTDG	180
181	FQFEYGGQGS	DPADVAIQLT	FLRLMSTEAS	QNITYHCKNS	VAYMDQQTGN	LKKALLLKGS	240
241	NEIEIRAEGN	SRFTYSVTVD	GCTSHTGAWG	KTVIEYKTTK	SSRLPIIDVA	PLDVGAPDQE	300
301	FGFDVGPVCF	L					

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 771 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pTrimer(T2)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 12..755
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

Hind III

BglII

AAGCTTACGTAAAGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCT
CAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCC

CGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACC
 CCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG
 CGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGAC
 AAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGG
 GCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTC
 CCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTC
 AAGAAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCT
 TCACCTACAGCGTCACTGTTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGAT
 TGAATACAAAACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGACGTTGGT
 GCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCTCCATCT
AGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

1	RSDANVVRDR	DLEVDTTLKS	LSQQIENIRS	PEGSRKNPAP	TCRDLKMCHS	DWKSGEYWID	60
61	PNQGCNLDAI	KVFCNMETGE	TCVYPTQPSV	AQKNWYISK	NPKDKRHVWFG	ESMTDGFQFE	120
121	YGGQGSDDPAD	VAIQLTFLRL	MSTEASQNIT	YHCKNSVAYM	DQQTGNLKKA	LLLKGSNEIE	180
181	IRAEGNSRFT	YSVTVDGCTS	HTGAWGKTVI	EYKTTKSSRL	PIIDVAPLDV	GAPDQEFQFD	240
241	VGPVCFL						

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pTrimer/AP-T0
(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 12..2471
 (D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

Hind III

AAGCTTCCTGC**ATG**CTGCTGCTGCTGCTGCTGCTGCTGGGCCTGAGGCTACAGCTCTCCCTG
GGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGCAGCCGAGGC
CCTGGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCT
TCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAG
AAGAAGGACAAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGC
TCTGTCCAAGACATAACAATGTAGACAAACATGTGCCAGACAGTGAGGCCACAGCCACGG
CCTACCTGTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGC
TTTAACCAGTGCAACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAA
GAAAGCAGGGAAAGTCAGTGGGAGTGGTAACCACCACACGAGTGCAGCACGCCTCGCCAG
CCGGCACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCC
TCGGCCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACAT
TGACGTGATCCTAGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCAGACCCTG
AGTACCCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAG
GAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCA
GGCTTCCCTGGACCCGTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGA
AATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCT
GCCCTGCGCCTGCTGAGCAGGAACCCCCGCGGCTTCTTCCTCTTCGTGGAGGGTGGTCG
CATCGACCATGGTCATCATGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGT
TCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACACGCTGAGCCTC
GTCACTGCCGACCACTCCACAGTCTTCTCCTTCGGAGGCTACCCCCTGCGAGGGAGCTC
CATCTTCGGGCTGGCCCCCTGGCAAGGCCCGGGACAGGAAGGCCTACACGGTCCTCCTAT
ACGGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGGCCGGATGTTACCGAGAGC
GAGAGCGGGAGCCCCGAGTATCGGCAGCAGTCAGCAGTGCCCCTGGACGAAGAGACCCA
CGCAGGCGAGGACGTGGCGGTGTTGCGCGCGGGCCCGCAGGCGCACCTGGTTCACGGCG
TGCAGGAGCAGACCTTCATAGCGCACGTATGGCCTTCGCCGCCTGCCTGGAGCCCTAC
ACCGCCTGCGACCTGGCGCCCCCGCCGGCACCAACCGACGCCGCGCACCCGGGTTCGGG
AAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTGCGACTGGTG
ATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGTCCTCCC
AGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCACGATGG
TGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGG
ACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGC
CGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAG
TGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCT
GCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAAG
AACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCAT

GACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCA
TCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCAC
TGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCT
CCTCAAGGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACA
GCGTCACTGTGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAA
TACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGG
TGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGT**TAA**ACTCCCT
CCATCTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

1	MLLLLLLLGL	RLQLSLGIIP	VEENPDFWN	REAAEALGAA	KKLQPAQTAA	KNLIIFLGDG	60
61	MGVSTVTAAR	ILKGQKKDKL	GPEIPLAMDR	FPYVALSKTY	NVDKHVPDSG	ATATAYLCGV	120
121	KGNFQTIGLS	AAARFNQCNT	TRGNEVISVM	NRAKKAGKSV	GVVTTTRVQH	ASPAGTYAHT	180
181	VNRNWYSAD	VPASARQEGC	QDIATQLISN	MDIDVILGGG	RKYMFPMTGP	DPEYPDDYSQ	240
241	GGTRLDGKNL	VQEWLAKRQG	ARYVWNRTTEL	MQASLDPSVT	HLMGLFEPGD	MKYEIHRDST	300
301	LDPSLMEMTE	AALRLLSRNP	RGFFLFVEGG	RIDHGHHSR	AYRALTETIM	FDDAIERAGQ	360
361	LTSEEDTSL	VTADHSHVFS	FGGYPLRGSS	IFGLAPGKAR	DRKAYTVLLY	GNGPGYVLKD	420
421	GARPDVTESE	SGSPEYRQOS	AVPLDEETHA	GEDVAVFARG	PQAHLVHGVQ	EQTFIAHVMA	480
481	FAACLEPYTA	CDLAPPAGTT	DAAHPGSGRS	NGLPGPIGPP	GPRGRTGDAG	PVGPPGPPGP	540
541	PGPPGPPSAG	FDFSFLPQPP	QEKAHDGGRY	YRADDANVVR	DRDLEVDTTL	KSLSQQIENI	600
601	RSPEGSRKNP	ARTCRDLKMC	HSDWKSGEYW	IDPNQGCNLD	AIKVFCNMET	GETCVYPTQP	660
661	SVAQKNWYIS	KNPKDKRHVW	FGESMTDGFQ	FEYGGQGSDF	ADVAIQLTFL	RLMSTEASQN	720
721	ITYHCKNSVA	YMDQQTGNLK	KALLLKGSNE	IEIRAEGNSR	FTYSVTVDGC	TSHTGAWGKT	780
781	VIEYKTTKSS	RLPIIDVAPL	DVGAPDQEFQ	FDVGPVCFL			

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2294 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pTrimer/AP-T2

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 12..2278

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

Hind III

AAGCTTCCTGC**ATG**CTGCTGCTGCTGCTGCTGCTGCTGGGCCTGAGGCTACAGCTCTCCCTG
GGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGCAGCCGAGGC
CCTGGGTGCCGCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCT
TCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAG
AAGAAGGACAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGC
TCTGTCCAAGACATAACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGG
CCTACCTGTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGC
TTTAACCAAGTGCAACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAA
GAAAGCAGGGAAGTCAGTGGGAGTGGTAACCACCACACGAGTGCAGCACGCCTCGCCAG
CCGGCACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCC
TCGGCCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACAT
TGACGTGATCCTAGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCAGACCCTG
AGTACCCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAG
GAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCA
GGCTTCCCTGGACCCGTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGA
AATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCT
GCCCTGCGCCTGCTGAGCAGGAACCCCCGCGGCTTCTTCCTCTTCGTGGAGGGTGGTCG
CATCGACCATGGTCATCATGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGT
TCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACACGCTGAGCCTC
GTCACTGCCGACCACTCCCACGTCTTCTCCTTCGGAGGCTACCCCTGCGAGGGAGCTC
CATCTTCGGGCTGGCCCCTGGCAAGGCCCGGGACAGGAAGGCCTACACGGTCTCCTAT
ACGGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGGCGGATGTTACCGAGAGC
GAGAGCGGGAGCCCCGAGTATCGGCAGCAGTCAGCAGTGCCCCTGGACGAAGAGACCCA
CGCAGGCGAGGACGTGGCGGTGTTGCGCGCGCGGCCCGCAGGCGCACCTGGTTCACGGCG
TGCAGGAGCAGACCTTCATAGCGCACGTGATGGCCTTCGCCGCTGCCTGGAGCCCTAC
ACCGCCTGCGACCTGGCGCCCCCGCCGGCACCAACCGACGCCGCGCACCCGGGTTCGGG
AGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAG
CCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCCC
GCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATT
GACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGG
TGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAAGTGGTACATCAGCA
AGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAG
TTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCT

GCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGG
 CCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGGCTCCAAC
 GAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTACCTACAGCGTCACTGTTCGATGG
 CTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACTAAGT
 CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAA
 TTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGT**TAA**ACTCCCTCCATCTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

1	MLLLLLLLGL	RLQLSLGIIP	VEEENPDFWN	REAAEALGAA	KKLQPAQTAA	KNLIIFLGDG	60
61	MGVSTVTAAR	ILKGQKKDKL	GPEIPLAMDR	FPYVALSKTY	NVDKHVPDSG	ATATAYLCGV	120
121	KGNFQTIGLS	AAARFNQCNT	TRGNEVISVM	NRACKAGKSV	GVVTTTRVQH	ASPAGTYAHT	180
181	VNRNWYSAD	VPASARQEGC	QDIATQLISN	MDIDVILGGG	RKYMFPMGTP	DPEYPDDYSQ	240
241	GGTRLDGKNL	VQEWLAKRQG	ARYVWNRTTEL	MQASLDPSVT	HLMGLFEPGD	MKYEIHRDST	300
301	LDPSLMEMTE	AALRLLSRNP	RGFFLFVEGG	RIDHGHHSER	AYRALTETIM	FDDAIERAGQ	360
361	LTSEEDTLSL	VTADHSHVFS	FGGYPLRGSS	IFGLAPGKAR	DRKAYTVLLY	GNGPGYVLKD	420
421	GARPDVTESE	SGSPEYRQOS	AVPLDEETHA	GEDVAVFARG	PQAHLVHGVQ	EQTFLAHVMA	480
481	FAACLEPYTA	CDLAPPAGTT	DAAHPGSGRS	DANVVRDRDL	EVDTTLKSL	QQIENIRSP	540
541	GSRKNPARTC	RDLKMCHSDW	KSGEYWDPN	QGCNLDAIKV	FCNMETGETC	VYPTQPSVAQ	600
601	KNWYISKPNK	DKRHVWFGES	MTDGFQFEYG	GQGSDDPADVA	IQLTFLRLMS	TEASQNITYH	660
661	CKNSVAYMDQ	QTGNLKKALL	LKGSNEIEIR	AEGNSRFTYS	VTVDGCTSHT	GAWGKTVIEY	720
721	KTTKSSRLPI	IDVAPLDVGA	PDQEFQFDVG	PVCFL			

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1734 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: pTrimer/sTNFR1I-T0
(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 18..1718
 (D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Bam HI

GGATCCCGCCCGCACCC**ATG**GGCGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCCGCCAGGTGGCATTACACCCTACGCCCCGGAGCCCGGG
AGCACATGCCGGCTCAGAGAATACTATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGC
CGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAGGA
CAGCACATACACCCAGCTCTGGAAGTGGGTTCCCGAGTGCTTGAGCTGTGGCTCCCGCTGTAGC
TCTGACCAGGTGGAACTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCG
GCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCG
CCCGGGCTTCGGCGTGGCCAGACCAGGAAGTGAACATCAGACGTGGTGTGCAAGCCCTGTGCC
CCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACG
TGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCACCCGGAG
TATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCCACACGATCCCAACACACGCAGCCA
ACTCCAGAACCCAGCACTGCTCCAAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAG
CTGAAGGGAGCACTGGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGG
TCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCC
CTGGTCCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAG
GCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGA
CCTCGAGGTGGACACCAACCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCC
CAGAGGGAAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCT
GACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCAT
CAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTG
TGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTC
GGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGC
CGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACA
TCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAG
AAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCG
CTTCACCTACAGCGTCACTGTGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGA
CAGTGATTGAATACAAAACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCC
TTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCT
GTAAACTCCCTCCATCTAGA

Xba I

- (2) INFORMATION FOR SEQ ID NO: 10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 566 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

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1  MAPVAVWAAL AVGLELWAAA HALPAQVAFT PYAPEPGSTC RLREYYDQTA QMCCSKCSPG    60
61 QHAKVFCTKT SDTVCDSCED STYTQLWNWV PECLSCGSRC SSDQVETQAC TREQNRICTC   120
121 RPGWYCALSK QEGCRLCAPL RKCRPGFGVA RPGTETSDVV CKPCAPGTFS NTTSSDICTR   180
181 PHQICNVVAI PGNASMDAVC TSTSPTRSMA PGAVHLPQPV STRSQHTQPT PEPSTAPSTS   240
241 FLLPMGPSPP AEGSTGSNGL PGPIGPPGPR GRTGDAGPVG PPGPPGPPGP PGPPSAGFDF   300
301 SFLPQPPQEK AHDGGRYRA DDANVVRDRD LEVDTTLKSL SQQIENIRSP EGSRKNPART   360
361 CRDLKMCHSD WKSGEYWIDP NQGCNLDAIK VFCNMETGET CVYPTQPSVA QKNWYISKNP   420
421 KDKRHWVFGE SMTDGFQFEY GGQGSDDPADV AIQLTFLRLM STEASQNTY HCKNSVAYMD   480
481 QQTGNLKKAL LLKGSNEIEI RAEGNSRFTY SVTVDGCTSH TGAWGKTIVIE YKTTKSSRLP   540
541 IIDVAPLDVG APDQEFGFDV GPVCFL

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(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: N
(iv) ANTI-SENSE: N
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(vii) IMMEDIATE SOURCE:
(B) CLONE: pTrimer/sTNFR1I-T2
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 18..1526
(D) OTHER INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

Bam HI

GGATCCCGCCCGCACCC**ATG**GCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCGCCAGGTGGCATTTACACCCTACGCCCCGGAGCCCGGG
AGCACATGCCGGCTCAGAGAATACTATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGC
CGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAGGA
CAGCACATACCCAGCTCTGGAAGTGGGTTCCCGAGTGCTTGAGCTGTGGCTCCCGCTGTAGC
TCTGACCAGGTGGAACTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCG

GCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCG
 CCCGGGCTTCGGCGTGGCCAGACCAGGAAGTGAACATCAGACGTGGTGTGCAAGCCCTGTGCC
 CCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACG
 TGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCACC GGAG
 TATGGCCCCAGGGGCAGTACACTTACCCCAGCCAGTGTCCACACGATCCCAACACACGCAGCCA
 ACTCCAGAACCCAGCACTGCTCCAAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAG
 CTGAAGGGAGCACTGGATCTGATGCCAATGTGGTTCTGTGACCGTGACCTCGAGGTGGACAC
 CACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCA
 AGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGA
 GAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAA
 CATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAAGT
 GGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACC
 GATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCA
 GCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCAGAACATCACCTACCACTGCA
 AGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTC
 AAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGT
 CACTGTGATGGCTGCACGAGTCAACCCGAGCCTGGGGCAAGACAGTGATTGAATACA
 AAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCC
 CCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTG**TAA**ACTCCCTCCAT
 CTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

1	MAPVAVWAAL	AVGLELWAAA	HALPAQVAFT	PYAPEPGSTC	RLREYYDQTA	QMCCSKCSPG	60
61	QHAKVFCTKT	SDTVCDSCED	STYTQLWNVW	PECLSCGSR	SSDQVETQAC	TREQNRICTC	120
121	RPGWYCALSK	QEGCRLCAPL	RKCRPGFGVA	RPGTETSDV	CKPCAPGTFS	NTTSSTDICR	180
181	PHQICNVVAI	PGNASMDAVC	TSTSPTRSMA	PGAVHLPQPV	STRSQHTQPT	PEPSTAPSTS	240
241	FLLPMGPSPP	AEGST GS DAN	VVRDRDLEVD	TTLKSLSQQI	ENIRSPEGS	RKNPARTCRDL	300
301	KMCHSDWKSG	EYWIDPNQGC	NLDAIKVFCN	METGETCVYP	TQPSVAQKNW	YISKPNPKDKR	360
361	HVWFGESMTD	GFQFEYGGQG	SDPADVAIQ	LFLRLMSTEA	QNITYHCKN	SVAYMDQQTG	420
421	NLKKALLLKG	SNEIEIRAEG	NSRFTYSVT	VDGCTSHTGAW	GKTVIEYKTT	KSSRLPIIDV	480
481	APLDVGPAPDQ	EFGFDVGPVC	FL				

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: N
- (iv) ANTI-SENSE: N
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pTrimer/sCD4-T0
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 24..2123
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

Hind III

AAGCTTCCCTCGGCAAGGCCACA**ATGA**ACCGGGGAGTCCCTTTTAGGCACTTGCTTCTG
GTGCTGCAACTGGCGCTCCTCCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAA
AAAAGGGGATACAGTGGAAGTACCTGTACAGCTTCCCAGAAGAAGAGCATACAATTCC
ACTGGAAAACTCCAACCAGATAAAGATTCTGGGAAATCAGGGGCTCCTTCTTAATAAAA
GGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAGGAAA
CTTTCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAG
TGGAGGACCAGAAGGAGGAGGTGCAATTGCTAGTGTTTCGGATTGACTGCCAACTCTGAC
ACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCCTTGGAGAGCCCCCTGGTAGTAG
CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGGAAGACCCTCT
CCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGCAGAAC
CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG
CATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCACTCGCCTTTACAG
TTGAAAAGCTGACGGGCAGTGGCGAGCTGTGGTGGCAGGCGGAGAGGGCTTCCTCCTCC
AAGTCTTGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGTACCCA
GGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCTGCCCCAGGCCT
TGCCTCAGTATGCTGGCTCTGGAAACCTCACCTGGCCCTTGAAGCGAAAACAGGAAAG
TTGCATCAGGAAGTGAACCTGGTGGTGTGAGAGCCACTCAGCTCCAGAAAAATTTGAC
CTGTGAGGTGTGGGGACCCACCTCCCCTAAGCTGATGCTGAGCTTGAACTGGAGAACA
AGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCTGAACCCTGAGGCGGGG
ATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCCTGCTGGAATCCAACATCAAGGT
TCTGCCCAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCA
CTGGTGATGCTGGTCTGTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGT
CCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCA
CGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCG

AGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAG
 GGAAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTG
 GAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAG
 TCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCC
 CAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGA
 GAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATG
 TGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACC
 TACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGC
 CCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCA
 CCTACAGCGTCACTGTGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTG
 ATTGAATACAAAACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGA
 CGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTG**TAAA**
 CTCCCTCCATCTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

1	MNRGVPFRLH	LLVLQLALLP	AATQGKKVVL	GKKGDTVELT	CTASQKKSIQ	FWWKNSNQIK	60
61	ILGNQGSFLT	KGPSKLNDR	DSRRSLWDQG	NFPLIIKNLK	IEDSDTYICE	VEDQKEEVQL	120
121	LVFGLTANS	THLLQGQSLT	LTLESPPGSS	PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	180
181	TWTCTVLQ	NQKKVEFKIDIV	VLAFAQASSI	VYKKEGEQVE	FSFPLAFTVE	KLTGSGELWW	240
241	QAERASSSKS	WITFDLKNKE	VSVKRVTDQ	KLQMGKKLPL	HLTLPQALPQ	YAGSGNLTLA	300
301	LEAKTGK	LHQEVNLVVMRAT	QLQKNLTCEV	WGPTSPKML	SLKLENKEAK	VSKREKAVWV	360
361	LNPEAGMWQC	LLSDSGQVLL	ESNIKVLPR S	<u>NGLPGPIGPP</u>	<u>GPRGRTGDAG</u>	<u>PVGPPGPPGP</u>	420
421	<u>PGPPGPPSAG</u>	<u>FDFSFLPQPP</u>	<u>QEKAHDGGRY</u>	<u>YRADDANVVR</u>	<u>DRDLEVDTTL</u>	<u>KSLSQQIENI</u>	480
481	RSPEGSRKNP	ARTCRDLKMC	HSDWKSGEYW	IDPNQGCNLD	AIKVFCNMET	GETCVYPTQP	540
541	SVAQKNWYIS	KNPKDKRHVW	FGESMTDGFQ	FEYGGQGS	ADVAIQLTFL	RLMSTEASQN	600
601	ITYHCKNSVA	YMDQQTGNLK	KALLLKGSNE	IEIRAEGNSR	FTYSVTVDGC	TSHTGAWGKT	660
661	VIEYKTTKSS	RLPIIDVAPL	DVGAPDQEF	GFDVGPVCF			

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1947 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: N
 (iv) ANTI-SENSE: N
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

 (vii) IMMEDIATE SOURCE:
 (B) CLONE: pTrimer/sCD4-T2
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 24..1931
 (D) OTHER INFORMATION:
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

Hind III

AAGCTTCCCTCGGCAAGGCCACA**ATGA**ACCGGGGAGTCCCTTTTAGGCACTTGCTTCTG
 GTGCTGCAACTGGCGCTCCTCCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAA
 AAAAGGGGATACAGTGGAAGTACCTGTACAGCTTCCAGAAGAAGAGCATACAATTCC
 ACTGGAAAACTCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTAATAAAA
 GGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAGGAAA
 CTTTCCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAG
 TGGAGGACCAGAAGGAGGAGGTGCAATTGCTAGTGTTTCGGATTGACTGCCAACTCTGAC
 ACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCCCTGGTAGTAG
 CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGGAAGACCCTCT
 CCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGACAGAAC
 CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG
 CATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCCTCGCCTTTACAG
 TTGAAAAGCTGACGGGCAGTGGCGAGCTGTGGTGGCAGGCGGAGAGGGCTTCCTCCTCC
 AAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGTACCCA
 GGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCTGCCCCAGGCCT
 TGCCTCAGTATGCTGGCTCTGGAAACCTCACCTGGCCCTTGAAGCGAAAACAGGAAAG
 TTGCATCAGGAAGTGAACCTGGTGGTGTGAGAGCCACTCAGCTCCAGAAAAATTTGAC
 CTGTGAGGTGTGGGGACCCACCTCCCCTAAGCTGATGCTGAGCTTGAAACTGGAGAACA
 AGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCTGAACCCTGAGGCGGGG
 ATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCCTGCTGGAATCCAACATCAAGGT
 TCTGCCCAGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCC
 TCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAAC
 CCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTA
 CTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG
 AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTAC
 ATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTTCGGCGAGAGCATGACCGATGG
 ATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGA

CCTTCCTGCGCCTGATGTCCACCGAGGCTCCCAGAACATCACCTACCACTGCAAGAAC
AGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGG
CTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTG
TCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACC
ACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGA
CCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTG**TAA**ACTCCCTCCATCTAGA

Xba I

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

1	MNRGVPFRHL	LLVLQLALLP	AATQGKKVVL	GKKGDTVELT	CTASQKKSII	Q FHWKNSNQIK	60
61	ILGNQGSFLT	KGPSKLNDRA	DSRRSLWDQG	NFPLIIKNLK	IEDSDTYICE	VEDQKEEVQL	120
121	LVFGLTANS	D THLLQGQSLT	LTLESPPGSS	PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	180
181	TWTCTVLQ	NQ KKVEFKIDIV	VLAFAQASSI	VYKKEGEQVE	FSFPLAFTVE	KLTGSGELWW	240
241	QAERASSSKS	WITFDLKNKE	VSVKRVTDQ	P KLQMGKKLPL	HLTLPQALPQ	YAGSGNLTLA	300
301	LEAKTGKLHQ	EVNLVVMRAT	QLQKNLTCEV	WGPTSPKLML	SLKLENKEAK	VSKREKAVWV	360
361	LNPEAGMWQC	LLSDSGQVLL	ESNIKVLPR	S DANVVDRDL	EVDTTLKSL	S QQIENIRSPE	420
421	GSRKNPARTC	RDLKMCHSDW	KSGEYWIDPN	QGCNLDAIKV	FCNMETGETC	VYPTQPSVAQ	480
481	KNWYISKNP	K DKRHVWFGES	MTDGFQFEYG	GQGSDDPADVA	IQLTFLRLMS	TEASQNITYH	540
541	CKNSVAYMDQ	QTGNLKKALL	LKGSNEIEIR	AEGNSRFTYS	VTVDGCTSHT	GAWGKTVIEW	600
601	KTTKSSRLPI	IDVAPLDVGA	PDQEFQFDVG	PVCFL			